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☐ 1: [AAA44992](#). envelope polyprot...[gi:328423]

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LOCUS AAA44992 854 aa linear VRL 02-AUG-1993  
 DEFINITION envelope polyprotein.  
 ACCESSION AAA44992  
 VERSION AAA44992.1 GI:328423  
 DBSOURCE locus HIVNL43 accession M19921.1  
 KEYWORDS .  
 SOURCE Human immunodeficiency virus 1 (HIV-1)  
 ORGANISM Human immunodeficiency virus 1  
 Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.  
 REFERENCE 1 (residues 1 to 854)  
 AUTHORS Adachi,A., Gendelman,H.E., Koenig,S., Folks,T., Willey,R.,  
 Rabson,A. and Martin,M.A.  
 TITLE Production of acquired immunodeficiency syndrome-associated  
 retrovirus in human and nonhuman cells transfected with an  
 infectious molecular clone  
 JOURNAL J. Virol. 59 (2), 284-291 (1986)  
 MEDLINE 86281827  
 PUBMED 3016298  
 REFERENCE 2 (residues 1 to 854)  
 AUTHORS Buckler,C.E., Buckler-White,A.J., Willey,R.L. and McCoy,J.  
 JOURNAL Unpublished (1988)  
 REFERENCE 3 (sites)  
 AUTHORS Dai,L.C., West,K., Littau,R., Takahashi,K. and Ennis,F.A.  
 TITLE Mutation of human immunodeficiency virus type 1 at amino acid 585  
 on gp41 results in loss of killing by CD8+ A24-restricted cytotoxic  
 T lymphocytes  
 JOURNAL J. Virol. 66 (5), 3151-3154 (1992)  
 MEDLINE 92219406  
 PUBMED 1373204  
 COMMENT [3] sites; revisions of [3].  
 Clean copy of sequence [3] kindly provided by Chuck Buckler, NIAID,  
 Bethesda, MD, 24-JUN-1988. The construction of pNL4-3 has been  
 described in [1]. pNL4-3 is a recombinant (infectious) proviral  
 clone that contains DNA from HIV isolates NY5 (5' half) and BRU (3'  
 half). The site of recombination is the EcoRI site at positions  
 5743-5748.  
 The length and sequence of the vpr coding region corresponds to  
 that of the BRU, SC, SF2, MAL and ELI isolates. The vpr coding  
 region of these isolates is about 18 amino acid residues longer  
 than the vpr coding region of the IIb isolates. In HIVNL43, this  
 shift is due to a single base deletion (with respect to the IIb's)  
 at position 5770. The sequence at this position is 'atttc' in  
 HIVNL43 and 'attttc' in HIVHXB2.  
 The original BRU clone, sequenced by Wain-Hobson, et al. (Cell 40,  
 9-17 (1985)), and the BRU portion of the pNL4-3 recombinant clone  
 are different clones from the same BRU isolate.  
 Two of the revisions reported in the FEATURES produced changes in  
 amino acid sequences. The revision at position 2421 changes one  
 amino acid residue from 'R' to 'G' in the pol coding region. The  
 revision at positions 8995-9000 changes three amino acid residues  
 from 'AHT' to 'VTP' in the nef coding region.

Method: conceptual translation.

FEATURES

	Location/Qualifiers
source	1..854 /organism="Human immunodeficiency virus 1" /db_xref="taxon:11676"
<u>Protein</u>	1..854 /name="envelope polyprotein"
<u>CDS</u>	1..854 /coded_by="M19921.1:6221..8785"

## ORIGIN

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1 mrvkekyghl wrwgwkwtm llgilmicsa teklwvtvvy gvpvwkeatt tlfcasdaka
61 ydtevhvwa thacvptdpn pqevvlvnt enfnmwkndm veqmhediiis lwdqslkpcv
121 kltpcvslk ctdlkndtnt nsssgrmime kgeikncsfm istsirdkvq keyaffykld
181 ivpidntsyr liscntsvit qacpkvsfep ipihycapag failkcnnkt fngtgpctnv
241 stvqcthgir pvvstqllln gslaeedvvi rsanftdnak tiivqlntsv einctrpnnn
301 trksirirgr pgrafvtigk ignmrqahcn israkwnatl kqiasklreq fgnnktiifk
361 qssggdpeiv thsfncggef fycnstqlfn stwfnstwst egsnntegsd titlpcrikq
421 finmwqevgk amyappisgq ircssnitgl lltrdggnnn ngseifrpqg gdmrdnwrse
481 lykykvvkie plgvaptkak rrvvqrekra vgigalflgf lgaagstmgc tsmtltvqar
541 qlldivqqq nllraieaq qhllqltvwg ikqlqarila verylkdqql lgiwgcsqkl
601 icttavpwna swsnksleqi wnnmtwmewd reinnytsli hsleesqng qekneqelle
661 ldkwaslwnw fnitnwlwyi klfimivggl vglrivfavl sivnrvrqgy splsfqthlp
721 iprgpdrpeg ieeeggerdr drsirlvngs laliwddlr lclfsyhrir dliivtriv
781 ellgrgwea lkywnllqy wsqelknsav nllnataiav aegtdrviev lqaayrairh
841 iprrirggle rill
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**1: AAB59751. envelope polyprot...**[gi:326424]

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LOCUS AAB59751 861 aa linear VRL 02-AUG-1993  
 DEFINITION envelope polyprotein.  
 ACCESSION AAB59751  
 VERSION AAB59751.1 GI:326424  
 DBSOURCE locus HIVBRUCG accession K02013.1  
 KEYWORDS  
 SOURCE Human immunodeficiency virus 1 (HIV-1)  
 ORGANISM Human immunodeficiency virus 1  
 Viruses; Retrovird viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.  
 REFERENCE 1 (residues 1 to 861)  
 AUTHORS Wain-Hobson,S., Sonigo,P., Danos,O., Cole,S. and Alizon,M.  
 TITLE Nucleotide sequence of the AIDS virus, LAV  
 JOURNAL Cell 40 (1), 9-17 (1985)  
 MEDLINE 85099333  
 PUBMED 2981635  
 COMMENT [(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor  
 Viruses,Molecu] review.  
 [3] revision of [1].  
 The original LAV, sometimes called LAV-1 to distinguish it from  
 HIV2 (LAV-2), is now referred to as HIV-1bru. An infectious clone  
 of this virus has been constructed by Keith Peden, Molecular Bio-  
 logy and Genetics, Johns Hopkins University School of Medicine,  
 Baltimore, MD 21205 (301) 955-3652. HIVNL43 is also an infectious  
 clone having for its 3' half a clone of the BRU isolate. Acquired  
 immune deficiency syndrome (AIDS) is caused by a retrovirus known  
 by several different names, probably representing two separate  
 strains: human T-cell lymphotropic virus-III (HTLV-III) and  
 lymphadenopathy-associated virus (LAV) are thought to be one  
 strain, and AIDS-associated retrovirus type 2 (ARV-2) the other.  
 All three viruses, whose sequences do not differ by more than about  
 6%, are believed to belong to the retroviral subfamily  
 Lentiviridae, or 'slow' viruses.  
 For the details of the annotation and for other pertinent  
 references, see the HIV reference entry.  
 Method: conceptual translation.  
 FEATURES Location/Qualifiers  
 source 1..861  
 /organism="Human immunodeficiency virus 1"  
 /db\_xref="taxon:11676"  
 Protein 1..861  
 /name="envelope polyprotein"  
 CDS 1..861  
 /coded\_by="K02013.1:5803..8388"

#### ORIGIN

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1 mrvkekyqhl wrwgkwgtm llgilmicsa teklwvtvvy gvpvwkeatt tlfcasdaka
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121 kltpclvslk ctdlgnatnt nssntnsssg emmmekgeik ncsfnistsi rgkvqkeyaf
181 fykldiipid ndttsytlts cntsvitqac pkvsfepipi hycapagfai lkcnnktfng
241 tgpctnvstv qcthgirpvv stqllngsl aeeevvirs nftdnaktii vqlnqsvein
301 ctrpnnntrk sirigrpgpr afvtigkign mrqahcnisr akwnatlkqi asklreqfgn
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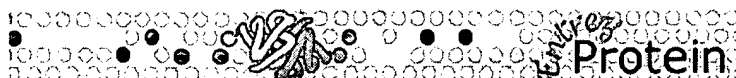
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421 lpcrikqfin mwqevgkamy appisggirc ssnitglllt rdggnnnngs eifrpgggdm  
481 rdnwrseelyk ykvvkieplg vaptkakrrv vqrekravgi galflgflga agstmgarsm  
541 tltvqarqll sgivqqqnnl lraieaqqhl lqltvwgikq lqarilaver ylkdqqligi  
601 wgcsgklict tavpwnasws nksleqiwnn mtwmewdreid nnytslihsd ieesqnqqek  
661 neqelleldk waslwnwfni tnlwlyikif imivgglvgl rivfavlsiv nrvrqqgyspl  
721 sfqthlptpr gpdrrpegiee eggerdrdrs irlvngslal iwddlrslcl fsyhrlrdll  
781 livtrivell grrgwealky wwnllqywsq elknsavsl1 nataiavaeg tdrvievvgg  
841 acrairhipr rirggleril 1

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☐ 1: [AAB59873](#). envelope polyprot...[gi:328559]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAB59873 856 aa linear VRL 01-OCT-1999  
 DEFINITION envelope polyprotein [Human immunodeficiency virus type 1].  
 ACCESSION AAB59873  
 VERSION AAB59873.1 GI:328559  
 DBSOURCE locus HIVPV22 accession [K02083.1](#)  
 KEYWORDS  
 SOURCE Human immunodeficiency virus 1 (HIV-1)  
 ORGANISM Human immunodeficiency virus 1  
 Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  
 lentivirus group.  
 REFERENCE 1 (residues 1 to 856)  
 AUTHORS Muesing,M.A., Smith,D.H., Cabradilla,C.D., Benton,C.V., Lasky,L.A.  
 and Capon,D.J.  
 TITLE Nucleic acid structure and expression of the human  
 AIDS/lymphadenopathy retrovirus  
 JOURNAL Nature 313 (6002), 450-458 (1985)  
 MEDLINE [85111157](#)  
 PUBMED [2982104](#)  
 REFERENCE 2 (sites)  
 AUTHORS van Beveren,C.P., Coffin,J. and Hughes,S.  
 TITLE Appendix B: HTLV-3/LAV genome  
 JOURNAL (in) Weiss,R.L., Teich,N., Varmus,H. and Coffin,J. (Eds.);  
 RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND  
 EDITION, 2: Supplements and Appendixes: 1106-1123;  
 Cold Spring Harbor Laboratory, CSH, NY (1985)  
 COMMENT [1] revised sequence, personal communication.  
 [(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.);RNA Tumor  
 Viruses,Molecu] review; bases 1 to 9769.  
 [3] revises [1],[ (in) Weiss,R., Teich,N., Varmus,H. and Coffin,J.  
 (Eds.);RNA Tumor Viruses,Molecu].  
 This sequence for a H9/HTLV-III virus was determined from one  
 complete proviral clone [1]. Additionally, several cDNA clones of  
 the viral RNA were sequenced for comparison with the entire  
 proviral sequence. The differences between cDNA and proviral DNA  
 are extensive and are listed in the Sites Table as variations. The  
 authors believe that the variations may be due in part to different  
 strains in the H9/HTLV-III cell line, because it was established by  
 infection with material from several AIDS patients. With the  
 addition of g at 2111, gag cds and pol cds are very close to those  
 of HXB2, BRU, and related HIV viruses.  
 For details and other references pertaining to Sites and Features,  
 see the HIV reference entry.  
 Method: conceptual translation.  
 FEATURES Location/Qualifiers  
 source 1..856  
 /organism="Human immunodeficiency virus 1"  
 /proviral  
 /db\_xref="taxon:11676"  
 Protein 1..856  
 /name="envelope polyprotein"  
 CDS 1..856  
 /coded\_by="K02083.1:6267..8837"

## ORIGIN

```
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61 ydtevhnvwa thacvptdpn pgevvlvntv enfnmwkndm vegmhediis lwdqslkpcv
121 kltplcvslk ctdlknndnt nsssgrmime kgeikncsfm istsirgkvq keyaffykld
181 iipidndtts ytltscntsv itqacpkvsf epipihycap agfailkcnn ktfngtgpct
241 nvstvqcthg irpvvstqll lngslaeeev virsanftdn aktiivqlnq sveinctrpn
301 nntrksirir rpggrafvti gkignmrqah cnisrakwnn tlkqidsklr eqfgnnktii
361 fkqssggdpe ivthsfncgg effycnstql fnstwfnstw stegsnnteg sdtitlpcrri
421 kqfinmwqev gkamyappis gqircssnit gllltrdggg nnneseifrp gggdmrdnwr
481 selykykvvk ieplgvaptk akrrvvqrek ravgigalfl gflgaagstm gaasmtltvq
541 arqllsgivq qqnnllraie aqqhllqltv wgikqlqari laverylkdq qllgiwgcsq
601 klicttavpw naswsnksle qiwnnmtwme wdreinnyts lihsleeesq nqgeknegcl
661 leldkwanlw nwnitnwlw yiklfimivg glvglrivfa vlsivnrvrq gysplsfqth
721 lptprgpdrr egieeedger drdrsirlvn gslaliwddl rslclfsyhr lrdlllivtr
781 ivellgrrgw ealkywnll qywsqelkns avsllnatai avaegtdrvi evvqgayrai
841 rhiprrirgg lerill
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